

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/656,811DATE: 08/21/96
TIME: 09:58:29

INPUT SET: S12262.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Bartsch, Dusan
Kandel, Eric R.
Ghirardi, Mirella

(ii) TITLE OF INVENTION: A METHOD FOR ENHANCING LONG-TERM MEMORY
IN A SUBJECT AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 50865/JPW/JML

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

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47 (B) TYPE: amino acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: linear
50

51 (ii) MOLECULE TYPE: peptide
52
53
54
55

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57

58 Met Glu Leu Asp Leu Trp Ser Glu Asp Phe Gln Leu Ala Arg Glu Trp
59 1 5 10 15
60

61 Gly Leu Glu Met Pro Val Val Gln Thr Asp Gly Gln Phe Gly Asp Leu
62 20 25 30
63

64 Lys Ser Thr Ser Arg His Gly Gly Asp Glu Ser Leu Ser Leu Gln Pro
65 35 40 45
66

67 Gln Gly Ala Thr Leu Lys Leu Glu Pro Phe Glu Glu Asp Val Leu Gly
68 50 55 60
69

70 Ala Glu Trp Met Glu Ser Ser Asp Leu Gly Ser Phe Leu Asp Ala Leu
71 65 70 75 80
72

73 Gly Asp Asn His Glu Arg Leu His Pro Phe Glu Ser Asn Leu Leu Glu
74 85 90 95
75

76 Phe Thr Ser Leu Ile Thr Pro Asp Asp Ser Thr Val Ser Lys Asp Ile
77 100 105 110
78

79 Leu Ser Ser Thr Leu Gln Phe Pro Thr Gln Pro Val Asn Ile Pro Leu
80 115 120 125
81

82 Tyr Ala Ser His Gly Ala Glu Asp Phe Ser Ala Glu Thr Glu Phe Glu
83 130 135 140
84

85 Asn His Leu Ser Pro Pro Asp Ser Pro Glu Gln Val Ala Pro Val Ile
86 145 150 155 160
87

88 Asn Leu Glu Pro Val Glu Leu Thr Ala Ser His Met Thr Val Ile Ser
89 165 170 175
90

91 Pro Asp Gly Leu Leu Gly Gly Met Glu Leu Ala Ser Glu Ser Leu Thr
92 180 185 190
93

94 Phe Thr Glu Leu Asp Phe Val Asn Phe Asn Asp Ser Ala Val Gly Ser
95 195 200 205
96

97 Ile Gly Gly Ala Glu Glu Leu Leu Gly Ser Pro Leu Ser Val Asp Asp
98 210 215 220
99

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100 Val Glu Ser Thr Ile Ser Phe Ser Gly Pro Ser Ser Pro Glu Thr Ser
101 225 230 235 240
102
103 Gln Ser Ser Ile Ile Glu Ser Ser Pro Glu Leu Tyr Lys Val Ile Ser
104 245 250 255
105
106 Thr Ser Ser Ile Asp Ala Ser Lys Arg Phe Ser Pro Tyr Ser Arg Ser
107 260 265 270
108
109 Ser Lys Ser Lys Gln Ser Val Lys Thr Ser Asp Ala Lys Ala Pro Arg
110 275 280 285
111
112 Lys Thr Arg Thr Pro Ala Gln Pro Val Pro Glu His Val Ile Met Glu
113 290 295 300
114
115 His Leu Asp Lys Lys Asp Arg Lys Lys Leu Gln Asn Lys Asn Ala Ala
116 305 310 315 320
117
118 Ile Arg Tyr Arg Met Lys Lys Lys Gly Glu Ala Gln Gly Ile Lys Gly
119 325 330 335
120
121 Glu Glu Gln Glu Leu Glu Glu Leu Asn Thr Lys Leu Lys Thr Lys Val
122 340 345 350
123
124 Asp Asp Leu Gln Arg Glu Ile Lys Tyr Met Lys Asn Leu Met Glu Asp
125 355 360 365
126
127 Val Cys Lys Ala Lys Gly Ile Gln Leu Lys Met
128 370 375
129
130

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

146 Leu Asp Lys Lys Asp Arg Lys Lys Leu Gln Asn Lys Asn Ala Ala Ile
147 1 5 10 15
148
149 Arg Tyr Arg Met Lys Lys Lys Gly Glu Ala Gln Gly Ile Lys Gly Glu
150 20 25 30
151
152 Glu Gln Glu Leu Glu Glu Leu Asn Thr Lys Leu Lys Thr Lys Val Asp

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153		35		40		45										
154																
155	Asp	Leu	Gln	Arg	Glu	Ile	Lys	Tyr	Met	Lys	Asn	Leu	Met	Glu	Asp	Val
156		50					55					60				
157																
158	Cys	Lys	Ala	Lys	Gly	Ile	Gln	Leu	Lys							
159		65					70									
160																
161																

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGACGTCA

8

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGTATTGCGT CATC

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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206
207
208
209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
210
211 ACTATTGCGC AATC 14
212
213 (2) INFORMATION FOR SEQ ID NO:6:
214
215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 20 base pairs
217 (B) TYPE: nucleic acid
218 (C) STRANDEDNESS: single
219 (D) TOPOLOGY: linear
220
221 (ii) MOLECULE TYPE: DNA (genomic)
222
223
224
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
227
228 TTCCGCTTTC CATAAGTCGA 20
229
230 (2) INFORMATION FOR SEQ ID NO:7:
231
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 20 base pairs
234 (B) TYPE: nucleic acid
235 (C) STRANDEDNESS: single
236 (D) TOPOLOGY: linear
237
238 (ii) MOLECULE TYPE: DNA (genomic)
239
240
241
242
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
244
245 ACCTGAAAAT GATATTGTAC 20
246
247 (2) INFORMATION FOR SEQ ID NO:8:
248
249 (i) SEQUENCE CHARACTERISTICS:
250 (A) LENGTH: 37 base pairs
251 (B) TYPE: nucleic acid
252 (C) STRANDEDNESS: single
253 (D) TOPOLOGY: linear
254
255 (ii) MOLECULE TYPE: DNA (genomic)
256
257
258

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SEQUENCE VERIFICATION REPORT
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Original Text